IN THE CLAIMS:

1. (currently amended) A method of using a mutation scanning array, wherein said mutation scanning array comprises a plurality of elements, wherein the elements contain immobilized oligonucleotides 8 - 50 bases long, that collectively span at least 10 different ~~whole~~ genes from the 5' to 3' end, wherein the genes can be either coding regions or the genomic genes, to identify mutations in a target DNA sequence which comprises:

(a) hybridizing the target DNA with a control DNA sequence to create a duplex, wherein the control DNA sequence is the wild-type DNA corresponding to the target DNA sequence,

(b) tagging any mismatch in said duplex with a detectable moiety,

(c) cleaving the duplex into segments of 50 - 300 bases,

(d) removing the segments tagged with the detectable moiety,

(e) contacting the segments tagged with the detectable moiety with the mutation scanning array, and

(f) identifying in which gene and gene segment the selected mismatch belongs to.

2. (currently amended) The method of claim 1 ~~claim 10~~, wherein the segments tagged with the detectable moiety are amplified before being used on the mutation scanning array.

3. (original) The method of claim 1 or 2, wherein the whole gene is represented by array elements; each element containing immobilized oligonucleotides that sample in 25-300 bases for the whole 3' to 5' mRNA sequence of each represented gene.

4. (currently amended) The method of claim 1 or 2, wherein each of the ~~whole~~ genes is represented by the coding ~~genomic~~ portion of the gene.

5. (currently amended) The method of claim 1 or 2, wherein each of the ~~whole~~ genes is represented by both the coding and non-coding genomic portions of a gene.

6. (currently amended) The method of claim 1 or 2, wherein said at least 10 different genes are ~~selected from the genome,~~ collectively known to predispose an individual to a particular disease.

7. (original) The method of claim 6, where the disease is a particular kind of cancer.

8. (original) The method of claim 6, where the disease is a cardiovascular abnormality, or a neurodegenerative disorder, or diabetes.

9. (currently amended) The method of claim 1 or 2, where said ~~the~~ genes ~~selected~~ are all known tumor suppressor genes or oncogenes.

10. (currently amended) The method of claim 1 or 2, where said ~~the~~ genes ~~selected~~ are genes known to be overexpressed in a malignant cell, wherein overexpression is determined by comparison to the gene's expression in a corresponding non-malignant cell.

11. (original) The method of claim 1, wherein the array is a chip or a microsphere.

12. (original) A method of using a mutation scanning array to identify mutation in a large DNA sequence, wherein said mutation scanning array comprises a plurality of elements, wherein the elements contain immobilized oligonucleotides 8 - 50 bases long, that collectively span at least 5 different genes, wherein said method comprises:

(a) hybridizing the target DNA sequence with a control DNA sequence wherein said control DNA sequence is the wild-type DNA sequence corresponding to the target DNA sequence to create a duplex;

(b) digesting the duplex to fragments of 50-300 base pairs, with restriction enzymes that allow generic addition of PCR primers;

(c) adding PCR primers to the duplex

(d) treating the duplex to remove any spontaneous aldehydes;

(e) reacting the duplex with a repair glycosylase to convert any mismatched sites in the duplex to reactive sites containing an aldehyde-containing abasic site;

(f) reacting the duplex with a compound of the formula X-Z-Y, wherein X is a detectable moiety, Y is NHNH2, O-NH2 or NH2, and Z is a hydrocarbon, alkyhydroxy, alkylethoxy, alkylester, alkylether, alkylamide or alkylamine, wherein Z may be substituted or unsubstituted; or where Z may contain a cleavable group; for a sufficient time and under conditions to covalently bind to the reactive sites;

(g) detecting the bound compound to identify sites of mismatches;

(h) isolating the DNA that contains mismatches from DNA without mismatches;

(i) PCR-amplifying the mismatch-containing DNA

(j) applying the mismatch-containing DNA on the Mutation Scanning Array, to determine the genomic position(s) where mismatches occur; and

k) determining whether the mismatch is a mutation or polymorphism.

13. (original) The method of claim 12, where the detectable moiety is selected from the group consisting of NH_2, SH, $NHNH_2$, a fluorescein derivative, a hydroxycoumarin derivative, a rhodamine derivative, a BODIPY derivative, a digoxigenin derivative and a biotin derivative.

14. (withdrawn)

15. (withdrawn)